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Genome-wide identification, evolutionary and expression analysis of the aspartic protease gene superfamily in grape

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Abstract

Background: Aspartic proteases (APs) are a large family of proteolytic enzymes found in almost all organisms. In plants, they are involved in many biological processes, such as senescence, stress responses, programmed cell death, and reproduction. Prior to the present study, no grape AP gene(s) had been reported, and their research on woody species was very limited.

Results: In this study, a total of 50 AP genes (*VvAP*) were identified in the grape genome, among which 30 contained the complete ASP domain. Synteny analysis within grape indicated that segmental and tandem duplication events contributed to the expansion of the grape AP family. Additional analysis between grape and *Arabidopsis* demonstrated that several grape AP genes were found in the corresponding syntenic blocks of *Arabidopsis*, suggesting that these genes arose before the divergence of grape and *Arabidopsis*. Phylogenetic relationships of the 30 *VvAP*s with the complete ASP domain and their *Arabidopsis* orthologs, as well as their gene and protein features were analyzed and their cellular localization was predicted. Moreover, expression profiles of *VvAP* genes in six different tissues were determined, and their transcript abundance under various stresses and hormone treatments were measured. Twenty-seven *VvAP* genes were expressed in at least one of the six tissues examined; nineteen *VvAP*s responded to at least one abiotic stress, 12 *VvAP*s responded to powdery mildew infection, and most of the *VvAP*s responded to SA and ABA treatments. Furthermore, integrated synteny and phylogenetic analysis identified orthologous AP genes between grape and *Arabidopsis*, providing a unique starting point for investigating the function of grape AP genes.

Conclusions: The genome-wide identification, evolutionary and expression analyses of grape AP genes provide a framework for future analysis of AP genes in defining their roles during stress response. Integrated synteny and phylogenetic analyses provide novel insight into the functions of less well-studied genes using information from their better understood orthologs.

Keywords: Synteny analysis, Phylogenetic analysis, Gene expression, Orthologous genes, Grape

Background

Aspartic proteinases (APs; EC 3.4.23) are widely distributed among living organisms, being found in plants, yeast, nematodes, parasites, fungi and even viruses. These enzymes have been extensively studied and constitute one of the four superfamilies of proteolytic enzymes [1-3]. APs

are usually characterized by the presence of two aspartic acid residues located within the conserved Asp-Thr/Ser-Gly motif responsible for catalytic activity [4]. They are active at acidic pH and are specifically inhibited by active site blockers such as pepstatin A, diazo-acetyl-norleucine methyl ester (DAN), and 1,2-epoxy-3-(p-nitro-phenoxy) propane (EPNP) [5]. APs are synthesized as single-chain preproenzymes which are subsequently converted to mature enzymes that can function as either monomeric or dimeric proteins during activation. According to the MEROPS database (<http://www.merops.ac.uk>), APs are now grouped into 14 different families on the basis of

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their amino acid sequence homology, evolutionary relationships, and tertiary structure; these groups in turn are assembled into six different clans [3]. Plant APs are distributed among several different families (A1, A3, A11 and A12 of clan AA, and family A22 of clan AD), but the majority belong to the A1 family [6].

Plant APs are classified as typical APs, nucellin-like APs and atypical APs [7]. Typical plant AP preproteins contain a C-terminal domain of approximately 50–100 amino acids (called the plant specific insert, PSI) which is removed during protein maturation. Neither their sequences nor structures share significant homology with animal or microbial APs; however, the PSI domain is homologous with the precursor of mammalian saposins [8]. The nucellin-like APs encode proteins similar to nucellin found in barley nucellar cells [9]. Atypical APs display intermediate features between the typical and nucellin-like sequences [7].

Plant APs have been implicated in protein processing and/or degradation in different plant organs. They are believed to play a role in plant senescence, stress responses, programmed cell death, and reproduction [6]. In contrast to APs of animal and microbial origin, plant APs are relatively poorly documented with regard to their biochemistry and physiological functions [10]. Furthermore, most of the analyses on plant APs have been performed in model species such as *Arabidopsis* [7,11], with little attention paid to woody species like grape.

Grapevine (*Vitis vinifera* L.) is one of the most important perennial fruit crops worldwide. It has been extensively studied at the physiological and developmental levels and was among the first fruits selected for full genome sequencing [12]. Compared to other perennials, the genome size of *V. vinifera* is relatively small (475 Mb) [12,13], which is similar to rice (*Oryza sativa*, 430 Mb) [14] and black cottonwood poplar (*Populus trichocarpa*, 465 Mb) [15]. In addition, the grapevine genome has not undergone a recent whole genome duplication (WGD), thus enabling the discovery of ancestral traits and genetic divergence occurring during the course of flowering plant evolution [12]. The release of grape genome data allows us for the first time to carry out the genome-wide identification and analysis of AP gene families in a woody species. Here we systematically identified 50 AP genes including 30 *VvAPs* that contain a complete ASP domain in the grape genome. Phylogenetic and synteny analyses revealed segmental and tandem duplication events that have contributed to the grape AP evolution. We further analyzed protein structures and exon/intron junctions of *VvAPs*. In addition, we determined the expression profiles of grape AP genes in six different tissues, and measured their transcript abundance in response to different phytohormone treatments and under various abiotic and biotic stresses. The results obtained from our study provide a foundation

for evolutionary and functional characterization of AP gene families in grape and other plant species.

Methods

Identification and annotation of grape AP genes

Grape AP genes were identified by searching grape proteins obtained from the Grape Genome Database (12×; <http://www.genoscope.cns.fr>) using the Hidden Markov Model (HMM) profile of ASP domain (PF00026) downloaded from the Pfam database (<http://pfam.sanger.ac.uk/>). The ASP domain in each identified AP gene was then manually checked for its completeness.

Determination of chromosomal localization and synteny analysis

The *VvAP* genes were positioned on grape pseudomolecules available at the Grape Genome Database (12 X). Tandemly duplicated AP genes in the grape genome were defined as adjacent to homologous AP genes on the grape chromosomes or within a sequence distance of 50 kb [16], with no more than one intervening gene [17]. For synteny analysis, synteny blocks within the grape genome and between grape and *Arabidopsis* genomes were downloaded from the Plant Genome Duplication Database and those containing grape AP genes were identified.

Sequence alignments and phylogenetic analysis

A total of 20 APs that lack a complete ASP domain, including *VvAP1*, *VvAP2*, *VvAP5*, *VvAP7*, *VvAP11*, *VvAP14*, *VvAP15*, *VvAP19*, *VvAP20*, *VvAP22*, *VvAP23*, *VvAP26*, *VvAP31*, *VvAP37*, *VvAP38*, *VvAP43*, *VvAP47*, *VvAP49* and *VvAP50*, were excluded from the phylogenetic analysis and further study. The remaining 30 *VvAPs* and *AtAPs* were aligned using ClustalX [18]. To compare and define subgroups, we integrated conserved ASP domain sequences of nucellins from barley (GenBank accession no. U87148) [9] into this dataset. The following *Arabidopsis* genes were selected for predicting the function of their orthologous counterparts in grape: *CDR1* (NP_198319, which plays a crucial role in activating resistance of *Arabidopsis* against microbial pathogens) [11]; *PCS1* (NP_195839, the PROMOTION of CELL SURVIVAL 1 gene, which encodes an aspartic protease with an important role in determining the fate of both male and female gametophytes and excessive cell death of developing embryos) [19]; and *ASPG1* (NP_188478, the ASPARTIC PROTEASE IN GUARD CELL 1 gene whose over expression conferred drought avoidance via ABA-dependent signalling in *Arabidopsis*) [20]. Phylogenetic trees were constructed with the MEGA 5.0 software using the neighbor-joining (NJ) method, and the bootstrap test was replicated 1000 times [21].

Exon/intron structure analysis of *VvAP* genes

The 30 *VvAP* genes with the complete ASP domain were used in this study. The Pfam domain and signal peptide were predicted using SMART (http://smart.embl-heidelberg.de/smart/set_mode.cgi?NORMAL=1) [22]. The diagram of protein structures was constructed with the DOG 1.0 software (<http://dog.biocuckoo.org/>) [23]. The exon/intron structures of the grape AP genes were determined from alignments of their coding sequences with corresponding genomic sequences using the est2genome program [24]. The diagram of exon/intron structures was obtained using the online Gene Structure Display Server (GSDS: <http://gsds.cbi.pku.edu.cn>) [25], which exhibited both exon position and gene length.

Plant materials

Grape tissues, including young roots, stems, leaves, and tendrils, flowers at the fully opening stage, and fruits at 33 days post anthesis were harvested from two year-old 'Kyoho' (*V. labrusca* × *V. vinifera*) seedlings grown in the field. 'Kyoho' was also used for high salt, drought stress, and exogenous hormone treatments. Chinese wild *Vitis quinquangularis* 'Shang-24' was used for powdery mildew inoculation. Both grape species are maintained in the grape germplasm resource orchard of Northwest A&F University, Yangling, China (34°20'N, 108°24'E).

Abiotic, hormone and biotic stress treatment

For abiotic stress, two year-old 'Kyoho' grape seedlings planted in pots were irrigated with 2 dm³ 250 mM NaCl [26,27]. After treatments for 1 h, 3 h, 6 h, 12 h, 24 h and 48 h, the fully unfolded young leaves were collected. Drought stress was carried out by withholding water from 'Kyoho' seedlings with some modification [28,29]. Briefly, young leaves of the seedlings were harvested at 24 h, 48 h, 72 h, 96 h, 120 h, 144 h and 168 h post treatment. Subsequently, the stressed plants were rewatered to soil saturation and leaves were collected at 48 h after rewatering. For salt and drought stress, plants watered every three days were used as control.

Hormone treatments were conducted by spraying young leaves with 100 μM SA [30,31] or 100 μM ABA [26,32] followed by sampling at 0.5 h, 1 h, 3 h, 6 h, 12 h, 24 h and 48 h post-treatment. Leaves sprayed with sterile distilled water at the same time points were collected as the control.

Pathogen treatment was carried out by inoculating the young leaves of 'Shang-24' with powdery mildew as previously described with minor modifications [33]. Prior to inoculation, leaves were sprayed with sterile water, and leaves were harvested at 6 h, 12 h, 24 h, 48 h, 72 h, 96 h and 120 h post-inoculation (Hpi). Control plants were simply sprayed with sterile water and not inoculated.

At each time point of each treatment, nine leaves from three separate plants were combined to form one sample. These leaves were immediately frozen in liquid nitrogen and stored at -80°C until use.

Several genes that have been reported to positively respond to abiotic or biotic stress were used to confirm the efficacy of the stress treatments; these included *RD22* and *CEF4* (induced by drought, salt and/or ABA treatments) [34-36], and *PR1* and *EDS1* (enhanced by SA treatment and powdery mildew inoculation) [37-40] (Additional file 1).

Semi-quantitative RT-PCR and real-time PCR analysis

Total RNA was extracted according to Zhang et al. [41], and then treated with 10 units of RNase-free DNase I (TaKaRa Bio Inc., Dalian, China) to remove genomic DNA contamination. For each sample, 1 μg of total RNA was used to synthesize first-strand cDNA using SuperScriptII reverse transcriptase (Invitrogen). For the following experiments, the reverse transcription products were diluted to six times. The concentration of the cDNAs was adjusted using the grape *Actin1* gene (GeneBank Accession number AY680701) with the primers F (5'-GAT TCT GGT GAT GGT GTG AGT-3') and R (5'-GAC AAT TTC CCG TTC AGC AGT-3') and the grape *EF1-α* gene (GeneBank Accession number EC931777) with the primers F (5'-AGG AGG CAG CCA ACT TCA CC-3') and R (5'-CAA ACC CTG CAT CAC CAT TC-3'). Gene-specific primers were designed for the 30 grape AP genes with the complete ASP domain (Additional file 2). For semi-quantitative reverse transcription-PCR (RT-PCR), a 20 μl reaction volume that included 1 μl of cDNA template, 1.6 μl of gene-specific primers (1.0 μM), 9.8 μl PCR Master Mix (Tiangen Biotech Co. Ltd., Beijing, China) and 7.6 μl sterile distilled water was used. The PCR parameters were 95°C for 3 min; followed by 25–35 cycles of 95°C for 30s, 58°C for 30s, 72°C for 25 s, and a final step at 72°C for 2 min. Each PCR was replicated three times. The results of semi-quantitative RT-PCR were quantified using the Gene Tools software, and the log-transformed values of the relative transcript abundance of *VvAP* genes under abiotic, hormone and biotic stress treatment compared to the control were used for hierarchical cluster analysis with Genesis software.

Quantitative real-time PCR analysis was conducted with an IQ5 real-time PCR instrument (Bio-Rad, Hercules, CA, USA). Each reaction was carried out in triplicate with a reaction volume of 20 μl containing 1.6 μl of gene-specific primers (1.0 μM), 1.0 μl of cDNA, 10 μl of SYBR green (TaKaRa Bio Inc.), and 7.4 μl sterile distilled water. The PCR parameters were 95°C for 30s, followed by 40 cycles of 95°C for 5 s and 60°C for 30s. Relative expression levels were analyzed using the IQ5 software and the normalized-expression method.

Database searches of the expression patterns of *AtAP* genes

The expression patterns of *AtAP* genes under powdery mildew infection and SA treatment were obtained from The Gene Expression Atlas of EMBL-EBI (<http://www.ebi.ac.uk/gxa/>) [42]. The expression patterns of these genes under salt and drought stresses and ABA treatment were obtained from Weigel World database (<http://jsp.weigelworld.org/expviz/expviz.jsp>) [43].

Targeting signals prediction of the grape AP genes

The targeting signals of grape AP genes were predicted with PSORT (<http://psort.hgc.jp/form.html>) [44].

Results

Genome-wide identification of AP genes in the *V. vinifera* genome

A total of 50 genes in the grape genome were identified as possibly AP genes (Table 1). Among them, 30 have the two complete Asp-Thr/ Ser-Gly motifs, while the others have either a single motif or an incomplete ASP domain. A total of 46 AP genes could be mapped to specific chromosomes and were named from *VvAP1* to *VvAP46* based on their order on the chromosomes (Figure 1, chromosomes 1–19). Four AP genes (GSVIVT01006876001, GSVIVT01006894001, GSVIVT01006895001 and GSVIVT01007227001) that could not be conclusively mapped to any chromosomes were named *VvAP47*–*VvAP50*, respectively. Furthermore, additional AP genes could also exist in the grape genome, awaiting identification by improved annotation methodology.

Expansion patterns of AP genes in grape

Segmental and tandem duplications are the main mechanisms leading to gene family expansions [45]. Thirty six AP genes involved in tandem duplications had been reported in rice [46]. In the present study, we also identified 11 tandemly duplicated AP genes (*VvAP3*/*VvAP4*, *VvAP5*–*VvAP8*, *VvAP22*–*VvAP24*, and *VvAP34*/*VvAP35* located on grape chromosomes 2, 4, 8 and 14, respectively) (Figure 1). Furthermore, we examined the segmentally duplicated blocks within the grape genome and found that there were 9 pairs of grape AP genes associated with segmental duplications (Figure 1), *VvAP10*/*VvAP34*, *VvAP16*/*VvAP44*, *VvAP40*/*VvAP18*, *VvAP42*/*VvAP17*, *VvAP27*/*VvAP45*, *VvAP32*/*VvAP21*, *VvAP13*/*VvAP25*, *VvAP22*/*VvAP14*, including two tandemly duplicated genes (*VvAP22* and *VvAP34*) (Additional file 3). In summary, half of the *VvAP* gene family members were associated with either segmental or tandem duplication events.

Evolutionary relationships of AP genes between grape and *Arabidopsis*

To further explore the origin and evolutionary process of grape AP genes, we analyzed the comparative synteny

map between grape and *Arabidopsis* genomes. *Arabidopsis* is among the most important model plant species, particularly with regard to AP genes since the functions of some of them have been well characterized. Thus through comparative genomics we can determine the origin and diversification of grape APs based on their *Arabidopsis* homologs.

Large-scale syntenies containing 23 AP genes in grape and 25 in *Arabidopsis* were identified (Figure 2). In addition, four genes in the *Arabidopsis* genome that were not annotated as AP genes were found to share synteny with grape AP genes (Additional file 4). Regarding the single grape-to-*Arabidopsis* AP gene correspondences, the syntenies were unambiguous and included the following orthologous pairs: *VvAP1*–*At1g25510*, *VvAP2*–*At5g47510*, *VvAP11*–*At5g19100*, *VvAP22*–*At3g52500*, *VvAP26*–*At1g79720*, *VvAP30*–*At4g30030*, *VvAP33*–*At3g54400*, *VvAP39*–*At1g49050*, *VvAP46*–*At3g12700*, indicating these genes should have been in the genome of the last common ancestor of grape and *Arabidopsis*. Among these, neither *At5g47510* nor *At5g19100* belonged to the *Arabidopsis* AP gene family; instead *At5g47510* has a SEC14 (domain in homologues of a *S. cerevisiae* phosphatidylinositol transfer protein) and a CRAL-TRIO-N (a protein structural domain that binds small lipophilic molecules) domain and *At5g19100* has a PDB domain 1T6G|B, both of which were also included in *VvAP2* and *VvAP11*, respectively. More challenging for syntenic interpretation were cases where grape segmental duplications corresponded to a single *Arabidopsis* gene or where a single grape gene corresponded to multiple *Arabidopsis* genes. The first situation included *VvAP13*/*VvAP25*–*At5g22850*, *VvAP13*/*VvAP25*–*At2g36670*, *VvAP16*/*VvAP44*–*At3g50050*, *VvAP17*/*VvAP42*–*At5g10080*, *VvAP18*/*VvAP40*–*At1g77480*, *VvAP21*/*VvAP32*–*At2g39710*, *VvAP21*/*VvAP32*–*At5g02190*, *VvAP27*/*VvAP45*–*At1g11910*, *VvAP27*/*VvAP45*–*At1g62290*, *VvAP27*/*VvAP45*–*At4g22050*; whereas the second included *VvAP13*–*At1g08210*/*At2g36670*/*At5g22850*, *VvAP21*–*At2g39710*/*At5g02190*, *VvAP25*–*At2g36670*/*At5g22850*, *VvAP27*–*At1g11910*/*At1g62290*/*At4g04460*/*At4g22050*, *VvAP31*–*At2g42980*/*At3g59080*, *VvAP32*–*At2g39710*/*At3g46620*/*At5g59550*/*At5g02190*, *VvAP37*–*At1g01300*/*At3g61820*, *VvAP40*–*At1g77480*/*At1g44130*, *VvAP44*–*At3g50050*/*At5g43100*, *VvAP45*–*At1g11910*/*At1g62290*/*At4g22050*. Among these, two of the four orthologs of *VvAP32* in *Arabidopsis* (*At3g46620* and *At5g59550*) were not AP genes; however, both of them had a RING and DUF1117 domain (data not shown), which could also be detected in *VvAP32*, implying that *VvAP32* may have undergone multiple significant chromosomal rearrangement and fusions. Finally, a third case was identified where two duplicated grape genes corresponded to multiple *Arabidopsis* genes. These were *VvAP13*/*VvAP25*–*At2g36670*/*At5g22850*, *VvAP21*/*VvAP32*–*At2g39710*/*At5g02190*, and *VvAP27*/*VvAP45*–*At1g11910*/*At1g62290*/*At4g22050*.

Table 1 AP genes in grape

Group	Gene	Gene locus ID	Accession no.	Chromosome	Start	End	Predicted gene length(bp)	Predicted ORF length(bp)
	VvAP1	GSVIVT01011932001	CBI27051.3	chr1	2921237	2927383	6147	771
	VvAP2	GSVIVT01001318001	CBI31923.3	chr2	5263175	5284039	20865	2346
C	VvAP3	GSVIVT01036932001	CBI29231.3	chr2	17430558	17432766	2209	927
C	VvAP4	GSVIVT01036930001	CBI29230.3	chr2	17439361	17448268	8908	1629
	VvAP5	GSVIVT01036013001	CBI21175.3	chr4	7189959	7192597	2639	1161
	VvAP6	GSVIVT01036015001	CBI21177.3	chr4	7244098	7247313	3216	1131
	VvAP7	GSVIVT01036017001	CBI21178.3	chr4	7263244	7279815	16572	1119
C	VvAP8	GSVIVT01036018001	XM_002268722	chr4	7315581	7317297	1717	1383
C	VvAP9	GSVIVT01019071001	XM_002277022	chr4	17094880	17107573	12694	1443
A1	VvAP10	GSVIVT01017701001	CBI26025.3	chr5	2775453	2778471	3019	1503
	VvAP11	GSVIVT01017894001	CBI26188.3	chr5	4453167	4455917	2751	1203
C	VvAP12	GSVIVT01031690001	CBI39464.3	chr5	20228612	20244419	15808	1434
C	VvAP13	GSVIVT01031432001	XM_002272085	chr6	18652672	18658561	5890	1455
	VvAP14	GSVIVT01036053001	CBI28265.3	chr6	21340808	21342747	1939	1341
	VvAP15	GSVIVT01028308001	CBI37099.3	chr7	5960288	5965597	5309	900
C	VvAP16	GSVIVT01000170001	CBI33735.3	chr7	15840160	15846953	6793	1902
C	VvAP17	GSVIVT01022186001	CBI21469.3	chr7	17268969	17274776	5807	1593
B	VvAP18	GSVIVT01022355001	XM_002273952	chr7	18933005	18936614	3610	1281
	VvAP19	GSVIVT01022392001	CBI21639.3	chr7	19580451	19581940	1490	837
	VvAP20	GSVIVT01025811001	CBI32837.3	chr8	11598470	11608650	10181	1368
C	VvAP21	GSVIVT01034136001	CBI30526.3	chr8	14910379	14911704	1326	1140
	VvAP22	GSVIVT01033940001	CBI30375.3	chr8	16541310	16569287	27978	771
	VvAP23	GSVIVT01033937001	CBI30373.3	chr8	16581910	16588393	6484	657
C	VvAP24	GSVIVT01033935001	CBI30372.3	chr8	16595281	16597123	1843	1338
C	VvAP25	GSVIVT01033723001	XM_002263093	chr8	18335899	18342508	6610	1509
	VvAP26	GSVIVT01016100001	CBI25263.3	chr9	18973023	18975323	2301	1080
A1	VvAP27	GSVIVT01012684001	XM_003632893	chr10	634034	638859	4826	1290
C	VvAP28	GSVIVT01026281001	CBI29076.3	chr10	15521671	15522975	1305	1305
C	VvAP29	GSVIVT01034372001	CBI35367.3	chr10	17284723	17286494	1772	1566
C	VvAP30	GSVIVT01010876001	XM_002265511	chr11	16540456	16541682	1226	1227
	VvAP31	GSVIVT01020842001	CBI22091.3	chr12	1179799	1181100	1301	1083
C	VvAP32	GSVIVT01016510001	CBI31649.3	chr13	3269121	3294047	24927	2286
C	VvAP33	GSVIVT01036671001	CBI35120.3	chr13	20059866	20062297	2431	963
A1	VvAP34	GSVIVT01031329001	XM_002276327	chr14	327811	331186	3376	1509
A1	VvAP35	GSVIVT01031327001	CBI39668.3	chr14	337889	340868	2980	1293
C	VvAP36	GSVIVT01019297001	CBI39998.3	chr15	1765842	1766963	1122	1005
	VvAP37	GSVIVT01027158001	CBI40559.3	chr15	17367842	17369993	2152	1311
	VvAP38	GSVIVT01024459001	CBI26572.3	chr16	2849198	2849563	366	366
B	VvAP39	GSVIVT01008267001	CBI15437.3	chr17	3799065	3805978	6913	1422
B	VvAP40	GSVIVT01008844001	CBI18999.3	chr18	2734587	2737586	3000	1173
C	VvAP41	GSVIVT01008883001	CBI19032.3	chr18	3102029	3103369	1341	1149
C	VvAP42	GSVIVT01008978001	CBI19115.3	chr18	3994150	4000643	6494	1566
	VvAP43	GSVIVT01009155001	CBI19249.3	chr18	5617213	5618770	1558	576
C	VvAP44	GSVIVT01009385001	XM_002283222	chr18	7918070	7925298	7229	1980
A1	VvAP45	GSVIVT01037685001	XM_002279013	chr19	6870994	6878047	7054	1545
C	VvAP46	GSVIVT01036694001	CBI24128.3	chr19	23803974	23806961	2988	1137

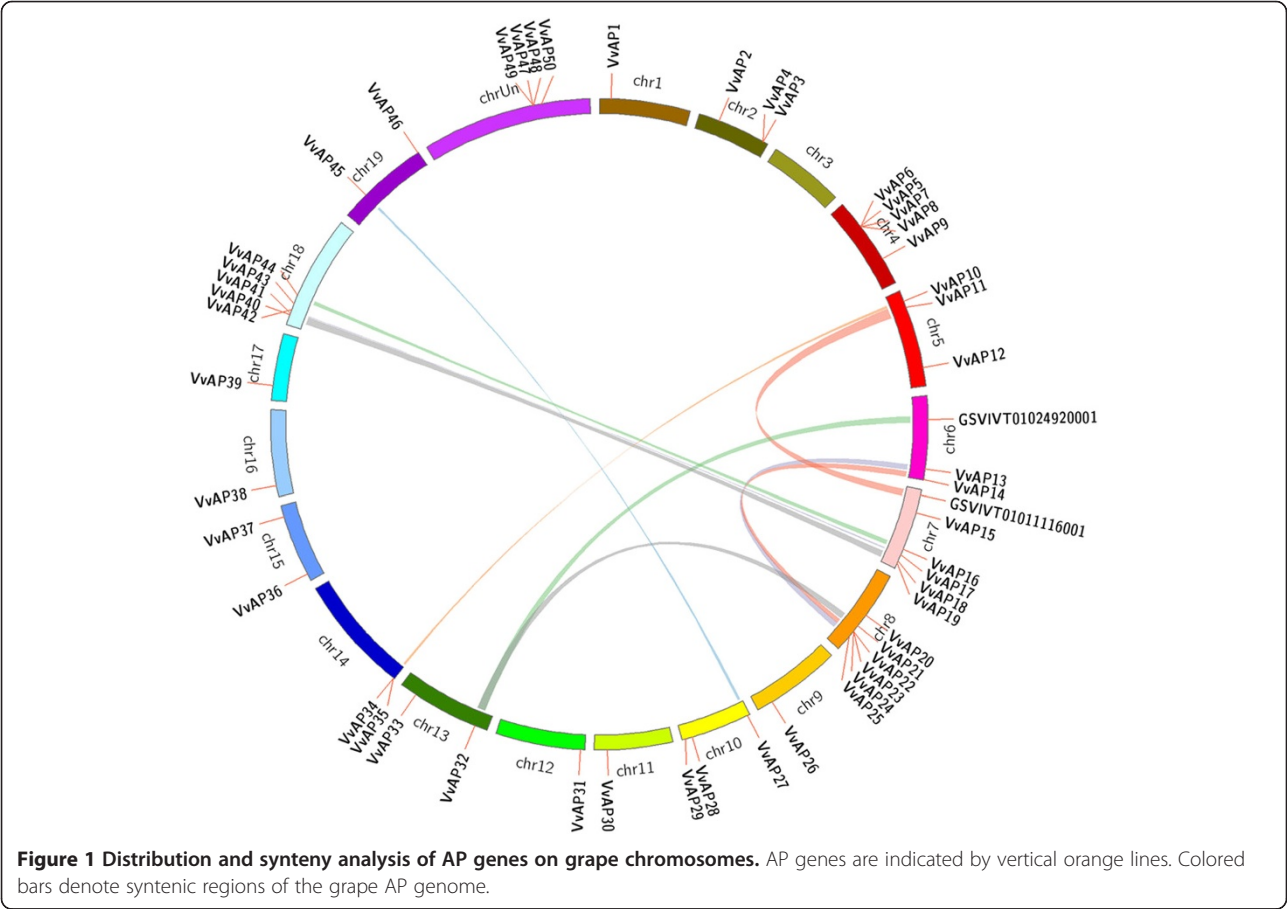
Table 1 AP genes in grape (Continued)

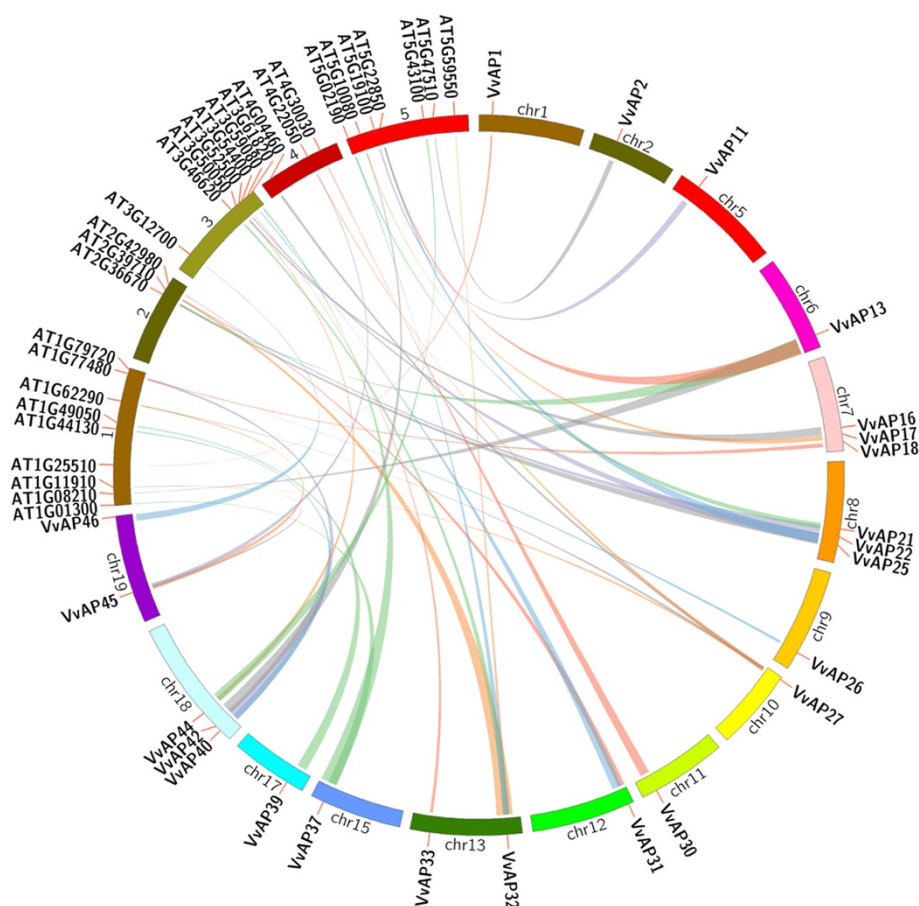
	VvAP47	GSVIVT01006876001	CBI29432.3	chrUn	28781234	28782604	1371	1011
C	VvAP48	GSVIVT01006894001	XM_002269844	chrUn	28931224	28934832	3609	1557
	VvAP49	GSVIVT01006895001	XM_003635291	chrUn	28936408	28937470	1063	450
	VvAP50	GSVIVT01007227001	CBI25840.3	chrUn	30964385	30966631	2247	906

Phylogenetic analysis of AP genes from grape and Arabidopsis

Among the 50 grape AP genes, 20 have an incomplete conservative ASP domain, and some of them can be mapped to synteny blocks between grape and Arabidopsis AP genes (*VvAP1*, *VvAP22*, *VvAP26*, *VvAP31* and *VvAP37*). As a result, we consider them to be members of the grape AP gene family. But since the main focus of this study was to investigate AP members bearing complete ASP domain, these 20 AP genes were therefore not used to construct the phylogenetic tree. The phylogenetic tree was constructed using the conserved ASP domain sequences of the remaining 30 grape AP genes and the *AtAPs*, as well as one family of reference genes (nucellins) (Figure 3). Three categories (A, B and C) were resolved, similar to those described in *Arabidopsis*

and rice [7,46]. Category A, which has been divided into A1 and A2 subgroups, containing five *VvAPs* and three *AtAPs* in A1, represented typical aspartic proteases. Two additional *AtAPs* (*At4g22050* and *At1g69100*) were included in subgroup A2; these genes do not have the PSI, but do possess other sequence elements that indicate they are more closely related to typical aspartic proteases than to any other sequences found in the *Arabidopsis* genome. Category B with three *VvAPs* and four *AtAPs* consisted of nucellin-like APs. Category C, composed of atypical aspartic proteases, was the largest group with 22 *VvAP* members and 43 *AtAP* members. Some researchers have divided category C further into five subgroups [7,46], but the criterion for classification was non-uniform, so in this study, the genes in category C were not classified further into subgroups. The rooted



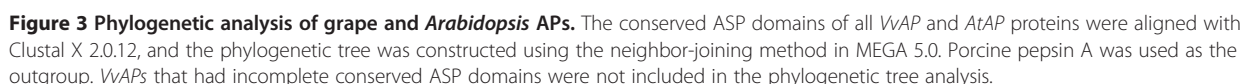


phylogenetic tree of ASP domains was also used to identify putative orthologs in *Arabidopsis* and grape (Additional file 5).

Sequence and structure analysis of grape AP genes

Phylogenetic analysis was also carried out using the conserved amino acid sequences of the 30 grape AP gene family members identified here (Figure 4A). The topology was similar to that constructed with AP sequences from grape and *Arabidopsis* (Figure 3) and, likewise, AP proteins from the same families within grape clustered together. One exception was the protein *VvAP24*, which had fallen into group C in the two-species analysis, while in the grape analysis it clustered together with the members of group A, being the most divergent member of the AP family.

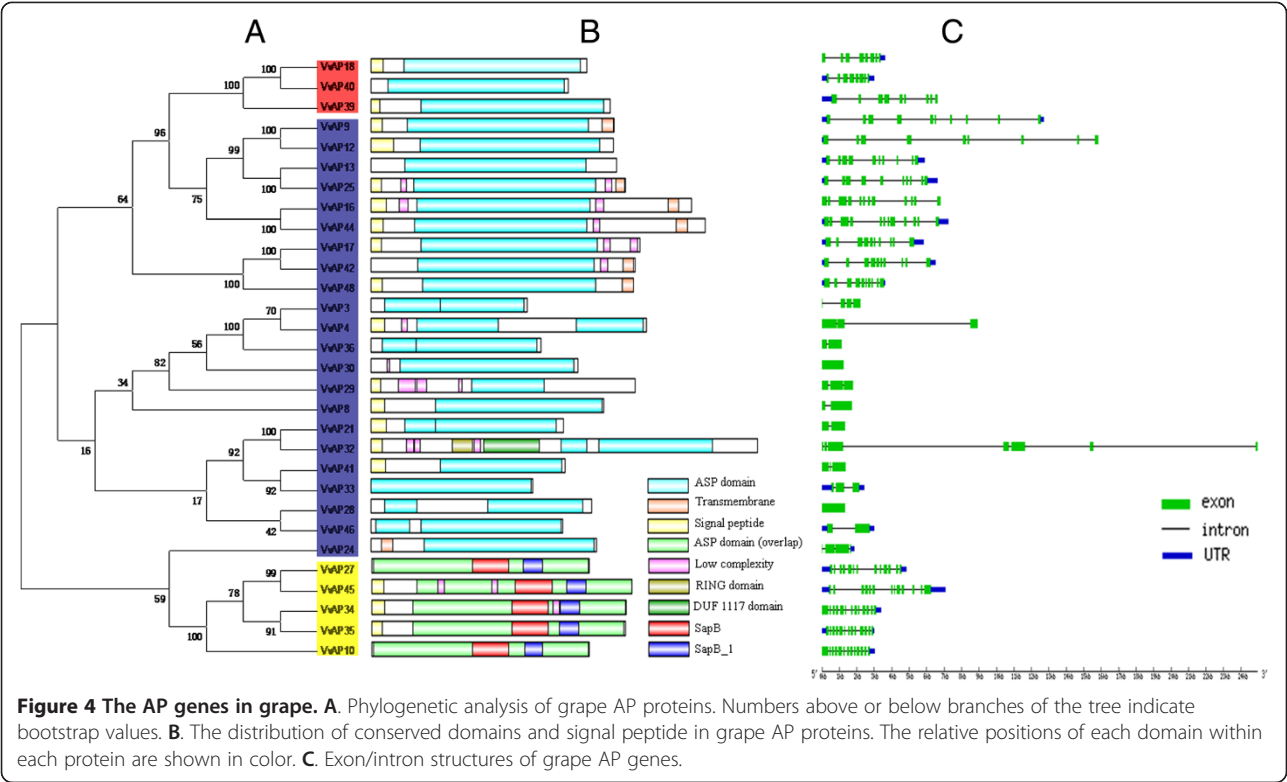
To provide further confirmation of the evolutionary relationships among the grape AP genes, we determined the distribution of their conserved domains (Figure 4B). By consensus, a *VvAP* protein has the following basic structure: a signal peptide, a propeptide, and an ASP domain with two active sites [47]. All of the 50 *VvAP*



Expression profiles of grape AP genes in different tissues
Semi-quantitative RT-PCR was used to detect the expression patterns of the 30 grape AP genes under normal growth conditions in six different tissues: roots, stems, leaves, flowers, fruits and tendrils. Of these, 27 genes (90%) were expressed in at least one of the six tissues (Figure 5). Expression of the other three genes (*VvAP4*, *VvAP30*, *VvAP41*) was not detected by RT-PCR in any of the tissues tested (data not shown). Twenty-one *VvAP* genes were expressed in all tested tissues but varied in expression levels. For example, *VvAP10* showed high levels of expression in roots, leaves and flowers, but much lower

Expression patterns of grape AP genes under different stress and exogenous hormone treatment conditions

Different approaches have been taken to improve plant stress tolerance, including manipulating and reprogramming the expression of endogenous stress-related genes. Therefore, identification and functional characterization of potential stress-related genes provides fundamental information for future improvement of plant stress tolerance. In the present study, we investigated the response



of grape AP genes to various abiotic and biotic stress conditions, as well as hormone treatments.

Abiotic stress

To determine whether *VvAP* genes are responsive to osmotic stresses in grape leaves, semi-quantitative RT-PCR was used to test their transcript abundance under salt and drought stress treatments. As shown in Figure 6 (see also Additional file 6, Additional file 7), 19 genes responded to at least one stress treatment. Three grape AP genes (*VvAP17*, *VvAP27* and *VvAP44*) exhibited enhanced transcript abundance by both treatments, whereas eight (*VvAP8*, *VvAP12*, *VvAP16*, *VvAP32*,

VvAP33, *VvAP34*, *VvAP35* and *VvAP46*) were down-regulated. In particular, the transcript abundance of *VvAP8*, *VvAP16*, *VvAP24*, *VvAP33*, *VvAP34* and *VvAP35* decreased gradually with the time under drought stress, while their transcript abundance increased after rewatering, while the other genes exhibited constitutive transcript abundance, or were up- or down-regulated. Interestingly, *VvAP25* was up-regulated in response to salt stress, but down-regulated in response to drought stress. In contrast, *VvAP28* and *VvAP39* transcript abundance decreased when treated with salt, but increased in response to drought. *VvAP13* was up-regulated when exposed to salt stress, while *VvAP10* exhibited decreased transcript

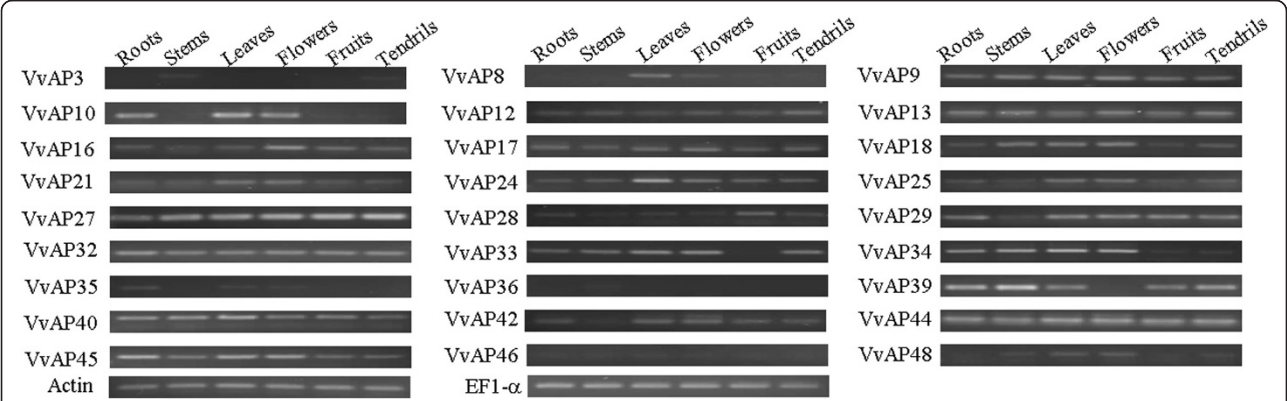


Figure 5 Expression profiles of 27 grape AP genes in various tissues as determined by semi-quantitative RT-PCR analyses.

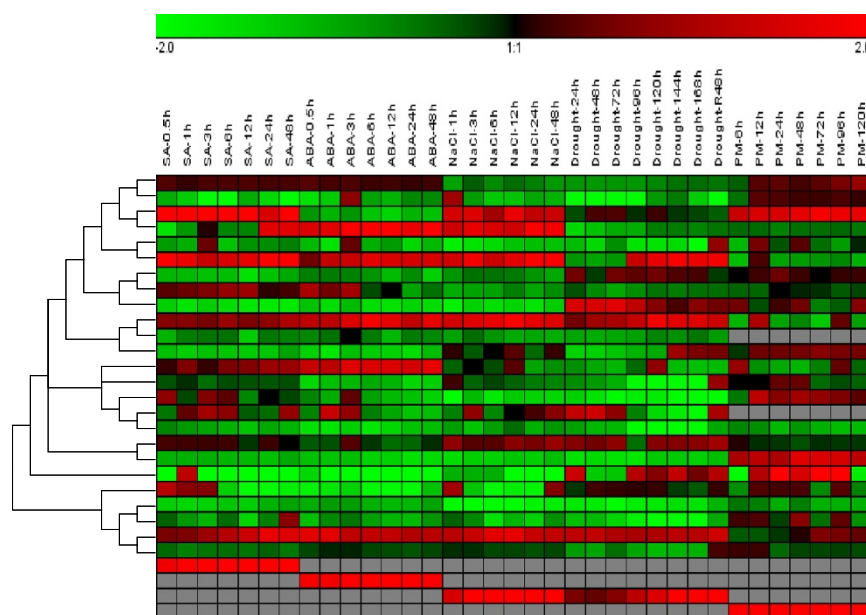


Figure 6 Hierarchical clustering of grape AP genes. The results of semi-quantitative RT-PCR were quantified using the Gene Tools software, and the log-transformed values of the relative expression levels of *VvAP* genes under SA, ABA, salt, drought and powdery mildew treatments compared to the controls were used for hierarchical cluster analysis with Genesis software (original results shown in Additional files 6, 7, 8, 9 and 10). The color scale represents relative expression levels with red as increased transcript abundance and green as decreased transcript abundance, gray in the figure represents not detected under the corresponding treatments. Sampling times are indicated at the top of the figure; R48 represents sampling 48 h after recovery from one week (168 h) of drought treatment.

abundance; these two genes were not affected by drought treatment. The transcript abundance of *VvAP8*, *VvAP24* and *VvAP45* were decreased by drought stress, but not affected by salt stress. The transcript abundance of the other six genes (*VvAP9*, *VvAP18*, *VvAP21*, *VvAP29*, *VvAP40*, *VvAP42*) was not regulated by either osmotic stress treatment. Transcript abundance of three randomly selected AP genes under either treatment were verified by real-time RT-PCR (Additional file 6B and Additional file 7B), indicating that the results of the real-time and semi-quantitative RT-PCR were consistent.

Biotic stress

Increasing evidence suggests that AP genes play important roles in response to pathogen infection [11,48]. The stress responses of the 30 grape AP genes were therefore investigated by semi-quantitative RT-PCR to obtain their transcript abundance under powdery mildew infection. *VvAP3*, *VvAP4*, *VvAP30*, *VvAP36* and *VvAP41* whose transcript abundance could not be detected in the leaves of 'Kyoho', were also not expressed in the leaves of 'Shang-24'. Neither *VvAP8* nor *VvAP42* were expressed in the mock leaves or in the inoculated leaves of 'Shang-24' (data not shown). Of the remaining 23 genes, half responded to powdery mildew infection, including *VvAP13*, *VvAP28*, *VvAP32* and *VvAP46* which were up-regulated and *VvAP16*, *VvAP17*, *VvAP25*, *VvAP29*, *VvAP33*, *VvAP34*,

VvAP35 and *VvAP44* which were down-regulated (Figure 6 and Additional file 8). The transcript abundance of *VvAP13* in infected leaves peaked at 72 h, whereas *VvAP32* increased slightly at 6 h and remained constant for the duration of the measurement period. *VvAP46* peaked at 12 h post-inoculation. Although the transcript abundance of *VvAP28* in infected leaves was weaker than in mock-inoculated leaves at 6 and 120 h post-infection, its transcript abundance was elevated from 12–96 h post-infection. The efficacy of semi-quantitative RT-PCR was also verified by determining the transcript abundance of three randomly selected AP genes under powdery mildew infection using real-time quantitative RT-PCR (Additional file 8B); both were in agreement.

Hormone treatment

The plant hormone, salicylic acid (SA), is a critical factor in plant responses to pathogen infection [49]. Analysis of transcript abundance from 'Kyoho' grape leaves sprayed with SA showed that seven of the 25 *VvAPs* (*VvAP13*, *VvAP17*, *VvAP25*, *VvAP27*, *VvAP29*, *VvAP40* and *VvAP44*) were up-regulated by different degrees upon treatment, whereas 11 *VvAP* genes (*VvAP12*, *VvAP16*, *VvAP18*, *VvAP28*, *VvAP32*, *VvAP33*, *VvAP34*, *VvAP35*, *VvAP39*, *VvAP42* and *VvAP48*) were down-regulated. *VvAP10* transcript levels were high at the first three sampling times after SA treatment, but declined thereafter (Figure 6 and Additional file 9).

ABA is known to play a central role in the response of plants to various types of abiotic stress [50]. Analysis of transcript abundance from 'Kyoho' leaves treated with exogenous ABA indicated that seven of the 25 *VvAP* genes analyzed exhibited increased expression at different times after treatment (Figure 6 and Additional file 10). For example, the transcript abundance of *VvAP17*, *VvAP25* and *VvAP44* was induced at 3 h after treatment, while that of *VvAP29* was essentially constitutive throughout the experiment. The transcript abundance of *VvAP8* peaked at 1 h after treatment, whereas both *VvAP27* and *VvAP40* peaked at 0.5 h post-treatment. Approximately half of the analyzed genes exhibited decreased transcript abundance, whereas the levels of *VvAP9*, *VvAP21*, *VvAP42* and *VvAP45* remained unchanged after treatment.

Discussion

Members of the plant AP family have been implicated in various physiological and developmental processes, including protein processing and degradation, senescence, stress response, programmed cell death and reproduction. However, virtually nothing is known about this family in woody species. Since grapevine is one of the most important fruit trees worldwide, and various forms of both biotic and abiotic stresses have a serious impact on its production and quality. Further study on stress-related responses in this genus could prove to be a significant asset. Therefore, we have sought to undertake the genome-wide identification of AP genes in grape, and provide clues regarding both their evolutionary histories and expression diversity with respect to stress-related conditions.

Tandem and segmental duplications contributed to the expansion of the grape AP gene family

Gene duplication, including tandem, segmental and whole genome duplications, has played an important role in the evolution of various organisms [51], and land plants have undergone abundant gene duplication throughout their evolutionary history [52]. Since the grapevine genome has not undergone any recent whole genome duplication events [12], segmental and tandem duplications would be the two main causes of gene family expansions in grape, although there is debate on the exact nature and timing of these events in grape [12,13]. In this study, 26 of 46 grape AP genes which could be precisely located on chromosomes were associated with either tandem or segmental duplication events (Figure 1 and Additional file 3), consistent with findings in rice whereby 51 of 93 AP genes were located in either tandemly or segmentally duplicated regions [46]. Taken together, this suggests that tandem and segmental duplications likely played an important role in the expansion of the AP family in plants. Although the duplicated grape AP genes identified here have a

common ancestor, we could not conclude from the work conducted here what the ancestral functions and expression patterns may have been, since gene duplication is considered to provide the raw material for evolution and duplicated genes which, if survive, could undergo substantial changes in their structures and/or regulatory mechanisms allowing them to assume novel roles [53].

The structural conservative and divergence of grape AP genes

Although several models of the genome evolution have been proposed from comparative genomic analyses of model organisms [54-56], little attention has been paid to the structural evolution of duplicated gene families [57]. In fact, exon/intron diversification of gene family members has played an important role in the evolution of multiple gene families through three main types of mechanism: exon/intron gain/loss, exonization/pseudo-exonization, and insertion/deletion [51]. It was obvious that grape AP genes within the same phylogenetic clade (Figure 4A) possessed highly similar exon/intron structures (Figure 4C) and most of the grape AP genes that clustered in the same phylogenetic clade were segmental or tandem duplications (Figure 1 and Figure 4A). Based on the results presented here, it is clear that the expansion of the grape AP family was the result of either segmental or tandem duplication. This is consistent with findings in rice [46], despite the fact that the numbers of exons of the *VvAP* genes in category C (1-4 or 9-12) were different from those of the *OsAP* genes in the same category (less than four).

Exon/intron gain/loss and divergence in exon/intron length which were observed within the coding sequences of several grape AP genes may be the result of chromosomal rearrangement and fusions. A good case was *VvAP32*, which had seven exons, but its paralogous gene, *VvAP21*, had just two exons. Moreover, *VvAP32* contained two other domains (RING and DUF1117) besides the ASP domain, and this might have resulted from a mechanism(s) leading to the additional exons. Divergence either in exon/intron length or exon/intron quantity could potentially lead to the generation of functionally distinct paralogs [51].

Functional conservation and divergence of tandem and segmental duplicated AP genes in grape

As discussed above, tandem and segmental duplication expanded the grape AP gene family, but it should be noted that only one gene in two of the four tandem duplicated paralogs (*VvAP5/VvAP6/VvAP7/VvAP8*, *VvAP22/VvAP23/VvAP24*) could be included in the phylogenetic tree (Figures 1 and 3), implying that sequences of these genes have been altered to a large extent after gene duplication,

and may therefore have lost their original functions or gained new ones.

The grape AP genes involved in the tandem and segmental duplication with complete ASP domains, clustered in the same phylogenetic clade (Figure 4A), and had highly similar exon/intron structures (Figure 4C); however, in different tissues and/or under a variety of stress or hormone treatments, the transcript abundance of the two genes within each pair of paralogs varied from each other (Figures 5 and 6). Although the expression patterns of *VvAP34* and *VvAP35* under each treatment were almost identical, different expression levels could be observed in the same plant organ. The expression of another pair of tandem duplicated paralogs, *VvAP3* and *VvAP4*, were barely detectable under the various treatments, but slight expression of *VvAP3* could be detected in the stems and tendrils of 'Kyoho'. Regarding the segmental duplication paralogs, almost all of the two AP genes within each pair of paralogs showed different transcript levels under three or four of the five treatments, and exhibited similar transcript abundance under the other one or two treatments. One exception was *VvAP17/VvAP42*, whose transcript levels were totally different under all of the five treatments. These results are similar to findings in rice [46], which showed that not all *OsAP* genes in the same category had similar expression patterns, and *OsAP* genes classified in the same expression pattern might have a distant phylogenetic relationship.

It seems possible that high sequence similarity is not necessarily correlated with similar transcript levels, because proteins with very similar sequences, presumably performing similar biochemical functions, are needed in different tissues and at different periods during growth and development, while at the same time responding to different stresses and hormone treatments. Similar transcript abundance exhibited by different AP genes with dissimilar sequences may perform different biochemical functions, suggesting they may work together in the tissues during growth and development or in response to the same stress or hormone treatment.

It has been reported that duplicated genes rarely diverge with respect to their biochemical function, but instead are limited to alterations in regulatory control [58]. So the different expression profiles between duplicated genes may be caused by varied regulatory network or mutations in the *cis*-regulatory regions [59], or mutations affecting the related regulatory network [60,61]. Epigenetic mechanisms, such as DNA methylation have also been suggested to potentially contribute to the expression divergence of duplicated genes [62,63], where transcriptional silencing has often been associated with DNA methylation in promoter regions [64,65].

A large part of expression divergence is considered to arise through duplication in the course of evolution [45],

and functional diversification of the surviving duplicated genes is also considered a major feature of the long-term evolution of polyploids [66]. It has been reported that four types of functional differentiation may follow gene duplication: pseudogenization, conservation of gene function, subfunctionalization and neofunctionalization [67]. Many duplicated genes may be lost from the genome after the duplication events, while neofunctionalization and subfunctionalization contribute to the retention of new genes. The *VvAP* gene family presents an opportunity to study how expression has diverged following gene duplication. Similar transcript abundance between duplicated genes, such as *VvAP34* and *VvAP35*, suggest that the regulatory mechanism of their expression have been conserved; on the other hand, divergence in expression patterns of the duplicated AP genes (neofunctionalization or subfunctionalization) could reflect the acquisition of novel regulatory mechanisms, while silencing of gene expression after duplication leading to nonfunctionalization of the gene implies drastic alteration of the regulatory mechanism.

Besides the possibilities that have been discussed above, the differences in specificity/catalytic properties and cellular localization among/between the duplicated genes could also contribute to the development of different biological functions, leading to the observed expression divergence [6,68,69]. It was found that almost all of the AP genes within each pair of paralogs were located in different parts of the cell, with two exceptions of *VvAP3/VvAP4* (both in the nucleus), and *VvAP17/VvAP42* (both in the plasma membrane) (Additional file 11). Even if these paralogs shared similar gene structure and cellular localization, the diversity of expression of these genes may be the result of alterations in regulatory sequences occurring shortly after duplication. In addition, alteration of function could also result from the presence or absence of protein-processing enzymes responsible for the activation/deactivation of the enzymes [6].

In summary, diversity in the transcript levels of the duplicated genes may be affected by different and multiple genetic factors depending on the causal duplication mechanism [70], and there maybe cross talk between different treatments or regulatory mechanisms. More research is needed to clarify the specifics of any functional divergence between grape duplicated AP genes, and new factors that may affect transcript divergence and how different factors work together are worth investigation.

The evolution of AP proteins in grape and *Arabidopsis* and functional prediction of grape AP genes

Genomic comparison is a quick way to transfer knowledge acquired in one taxon for which there is a better understanding of genome structure and function to a

less-studied taxon [71]. Thus, the richness of gene functional information known for model plants such as *Arabidopsis* enables one to extrapolate functions of their orthologous genes in other plant taxa. To obtain an overall picture of the grape AP proteins and their relationships with those of *Arabidopsis*, both syntenic and phylogenetic analyses have been performed, and the evolutionary relationship of this gene family within and among the different species has been systematically studied.

There were 23 grape and 25 *Arabidopsis* AP genes, as well as the other four *Arabidopsis* genes that were syntenic orthologous (Figure 2, Additional file 4). Among these, 10 were single grape-to-*Arabidopsis* AP orthologs, indicating these genes come from a common ancestor. The other genes constituted a more complex situation, including ten cases of two grape AP genes that corresponded to one *Arabidopsis* AP gene, 10 cases of one grape AP gene corresponding to multiple *Arabidopsis* AP genes, and three cases of two duplicated grape AP genes that corresponded to multiple *Arabidopsis* AP genes. Certainly, most of the genes included in the complex situation appeared more than once. For example, *VvAP27* correspondence to *At1g11910* and *At1g62290* located on the Chr1 of *Arabidopsis*, as well as *At4g04460* and *At4g022050* located on the Chr4 of *Arabidopsis*, and *VvAP45* correspondence to *At1g11910*, *At1g62290* and *At4022050*, but not to *At4g04460*, so it is impossible to elucidate whether divergence of *VvAP27* and *VvAP45* located in segmental duplications of grape and *At1g11910*, *At1g62290*, *At4022050* and *At4g04460* in *Arabidopsis* occurred prior to or after the divergence of grape and *Arabidopsis* from the last common ancestor. Although 27 grape AP genes could not be mapped into any syntenic blocks, we could not conclude that these genes from grape and *Arabidopsis* did not share a common ancestor. This may be explained by the fact that after the divergence of lineages that led to grape and *Arabidopsis*, their genomes underwent multiple rounds of significant chromosomal rearrangement and fusions, followed by selective gene loss, which can severely obscure the identification of chromosomal syntenies [72]. In such case, it maybe concluded that some of the AP genes in grape and *Arabidopsis* come from a common ancestor, while the others do not. Although the evolutionary histories of grape AP genes could not be established for the period prior to the split between grape and *Arabidopsis* lineages, at least some of the grape genes appeared to share a common ancestor with their *Arabidopsis* AP counterparts.

In order to improve prediction of the functions of specific grape AP genes based on the reported function of their *Arabidopsis* homologs, a phylogenetic tree was constructed, and bootstrap support values (1000 re-sampling) exceeding 50% were used to identify possible orthologous

pairs (Figure 3). For example, *VvAP30* and *At4g30030* were clustered together in the phylogenetic tree, but the bootstrap value of their node was no more than 50%. Therefore, *VvAP30* and *At4g30030* were excluded from the orthologous pairs, as were *VvAP13* and *At1g08210/At5g22850*, *VvAP16/VvAP44* and *At3g50050*, *VvAP27* and *At4g04460*, *VvAP17/VvAP42* and *At5g10080*, *VvAP46* and *At3g12700*. There were 11 orthologous pairs in the phylogenetic tree that could not be detected in the syntenic orthologs, and 21 syntenic orthologs that could not be detected or were not clustered together in the phylogenetic tree (Additional file 4, Additional file 5, Additional file 12). Thus, there were ten orthologs including 8 grape AP genes (*VvAP27/VvAP45-At1g11910/At1g62290*, *VvAP39-At1g49050*, *VvAP21-At5g02190*, *VvAP25-At2g36670*, *VvAP32-At2g39710*, *VvAP33-At3g54400* and *VvAP44-At5g43100*) that could be clustered together in the phylogenetic tree and were also contained in the syntenic map (Additional file 5, Additional file 12). Expression patterns of the ten orthologs were more similar than other orthologous pairs that only clustered together in the phylogenetic tree or were syntenic orthologs (Additional file 12). As a result, we can speculate that the functions of the eight grape AP genes are more similar to their *Arabidopsis* homologs than the other grape APs in the phylogenetic tree and syntenic map. Ling et al. [73] has used phylogeny-based methods to identify orthologs between *Arabidopsis* and cucumber, and further analyzed the correlation of roles of orthologous pairs under abiotic stresses. Their results showed that correlative expression profiles in stress-inducible orthologous WRKY genes between cucumber and *Arabidopsis* and orthologous WRKY genes with different evolutionary patterns displayed a low correlation in their expression patterns [73]. Our study combining synteny analysis with a phylogenetic tree provides new insight for investigating the function of grape AP genes by comparing orthologous genes between two plants, in one of which functional roles for the genes have been identified, in this case, between grape and *Arabidopsis*.

VvAP proteins play important roles in a range of biological processes

It has been reported that plant APs are implicated in a variety of biological processes [6,7]. The study on the rice AP gene family showed that 66 genes were presented in at least one of the developmental stages analyzed [46]. Timotijevic et al. [74] isolated an aspartic proteinase gene *FeAP12* from developing buckwheat seeds, and found the gene was seed-specifically expressed. Moreover, the highest levels of *FeAP12* expression were observed in the early stages of seed development, suggesting a potential role in nucellar degradation [74]. Our RT-PCR results showed that most of the *VvAP* genes exhibited diverse

expression levels in all six organs, indicating these APs often participate in plant development. Genes which showed higher expression levels in one organ than in others may play key roles in the development process of the corresponding organ. It was worth noting that the expression of *VvAP36* could only be detected in stems, indicating its potential role in the stem development.

Evidence is accumulating that AP proteins are involved in plant responses to various abiotic and biotic stresses. Cruz et al. [75] reported that in drought-susceptible common bean cultivars subjected to water deficit, the expression of an AP gene was shown to be transcriptionally up-regulated and its activity was significantly increased. In recently published reports, Yao et al. [20] have shown that an *Arabidopsis* gene, *ASPG1* (*aspartic protease in guard cell 1*), may function in drought avoidance through abscisic acid (ABA) signaling in guard cells. An aspartic protease gene, *FeAP9*, whose expression was up-regulated in leaves under different abiotic stresses has also been found in developing organs of buckwheat [69]. In the present study, we showed that 18 *VvAP* genes exhibited differential transcript abundance in response to at least one abiotic stress (Figure 6), indicating that *VvAP* genes may play an important role in protecting grape from abiotic stresses.

Expression of an extracellular AP gene has also been detected in tobacco and tomato leaves and implicated in the degradation of pathogenesis-related (PR) proteins. It has been suggested that APs may play a role in a conserved mechanism for PR-protein turnover, preventing over accumulation and thereby regulating the biological functions of these stress induced proteins [76,77]. These APs were also shown to be constitutively expressed either in healthy or infected leaves, which was consistent with our findings in this study. Studies with potato showed that the expression levels of *StAPs* were associated with the degree of resistance of potato cultivars to *Phytophthora infestans*, and potato aspartic proteinases were components of the plant defense response [78]. Xia et al. [11] have also shown the accumulation of an AP gene, *CDR1* (*Constitutive disease resistance*), in response to pathogen attacks. The *CDR1* gene in rice has also been studied, and the results suggested that *OsCDR1* was implicated in disease resistance signaling [10]. Powdery mildew, caused by the obligate biotrophic fungus, *Uncinula necator*, has a serious impact on grape productivity and fruit quality [79]. As shown in Figure 6, four of the grape AP genes exhibited increased transcript abundance in the infected leaves, indicating these genes may participate in the plant response to powdery mildew infection. It has been reported that the PSI may take part in defensive mechanisms against pathogens and/or as an effector of cell death [6], but none of the grape AP genes in group A1 was up-regulated upon powdery mildew infection. However, we

cannot conclude that the *VvAPs* in group A1 have no function in defensive against pathogens, because they may participate in resistance against other pathogens.

Besides the functions of APs in response to abiotic and/or biotic stress, some APs were reported to be involved in PCD (programmed cell death) [80]. In addition, nucellin, an AP belonging to group B subfamily and known to be expressed specifically in nucellar cells during degeneration after ovule fertilization in barely, was suggested to be involved in PCD [9]. So we can speculate that *VvAPs* in group B is also involved in various types of PCD [81].

Differences of the cellular localization of AP genes may result in their different biological functions [6,68,69], and it has been reported that most plant APs were vacuolar enzymes [82-85], or were secreted to the cell wall [86,87]. But there were many aspartic proteinases in *Arabidopsis* and one third of the grape AP genes were predicted to be localized to the chloroplast and chloroplast thylakoid membrane, respectively [7] (Additional file 11). In tobacco, one chloroplast-located AP gene named *CND41* (for 41 kD Chloroplast Nucleoid DNA-binding protein) is involved in degradation of the Rubisco holoprotein during leaf senescence, and the accumulation of *CND41* is negatively correlated with chloroplast transcript levels in tobacco cells [88-90]. The homologs of *CND41* in *Arabidopsis* have also been confirmed to participate in the regulation of Rubisco turnover and senescence [91-93]. In a more recently published report, Paparelli et al. [94] have identified a chloroplast-located AP gene *NANA* whose misexpression or overexpression not only influences photosynthetic carbohydrate metabolism but also plastid and nuclear gene expression [94]. So the localization of these AP genes to the *Arabidopsis* or grape thylakoid membranes raises the possibility that they may fulfill roles as specific processing enzymes in this organelle, or participate in maintenance or degradation of photosystem proteins [7,95].

To get a more complete understanding of the biological functions of the AP gene family, identification of substrates that AP proteins act on and the regulatory network of AP genes participating in response to various pathogens are necessary. The results presented here indicate that the regulatory role of AP proteins under abiotic and biotic stress is complex and more work is needed to understand the regulatory mechanisms.

Conclusions

In the present study, we identified a total of 50 grape AP genes, 30 of which had complete ASP domains. Synteny analysis within grape demonstrated that segmental and tandem duplications have contributed to the expansion of the grape AP gene family. Comparative synteny analysis between the *V. vinifera* and *Arabidopsis* genomes indicated that some of the grape and *Arabidopsis* AP

genes were located in syntenic regions, suggesting that these genes had common ancestors. Separation of the grape AP genes into three groups was mutually supported by their phylogeny, exon/intron structure and the distribution of conserved domains. Finally, we analyzed expression profiles of 30 *VvAP* genes that possess a complete ASP domain under normal growth conditions and in response to various abiotic and biotic stresses and hormone treatments. Some of the genes evaluated were not expressed in leaves of 'Kyoho' and/or 'Shang-24'. The expression information reported here will be useful for further investigation of the function of AP genes under various stress conditions. Although the genome sequence of grape has been reported, functional studies on grape genes still lag behind. We integrated the synteny analysis between grape and *Arabidopsis* with a phylogenetic tree of the two species, and found that there were ten orthologs, including eight grape AP genes clustered together in the phylogenetic tree and also contained in the syntenic map. Although correlation of the expression of orthologous AP genes in grape and *Arabidopsis* was not calculated, the method of combining synteny analysis with the phylogenetic tree may provide a new approach for investigating gene function from their orthologs whose functions have been previously clarified. These studies could increase our understanding of the roles of these genes in grape, but further functional analysis of stress-responsive *VvAPs* is required to confirm their role in stress tolerance.

Additional files

Additional file 1: The primer sequences used for semi-quantitative RT-PCR of the selected positive control genes for salt, drought, powdery mildew, SA and ABA treatments. The specific primers were obtained from published reports.

Additional file 2: The primer sequences used for semi-quantitative RT-PCR amplification of 30 *VvAP* genes. The specific primers were designed according to the AP gene sequence by Primer 5.0 software.

Additional file 3: Synteny blocks of AP genes within the grape genome. The data were downloaded from the Plant Genome Duplication Database, and those containing grape AP genes were identified.

Additional file 4: Synteny blocks of AP genes between grape and *Arabidopsis* genomes. The data were downloaded from the Plant Genome Duplication Database, and those containing grape AP genes were identified.

Additional file 5: Putative orthologs of grape and *Arabidopsis*. Grape AP proteins and their putative orthologs in *Arabidopsis* were identified based on phylogenetic studies of ASP domain sequences.

Additional file 6: Expression patterns of grape AP genes under salt treatment condition. A. Expression patterns of 25 AP genes under salt treatment conditions were determined by semi-quantitative RT-PCR analyses. For each gene, the upper six amplification bands represent amplified products from leaves of 'Kyoho' after treatment with 2 dm³ 250 mM NaCl; the bands under them represent amplified products from leaves of the control. B. Expression patterns of three randomly selected AP genes were analyzed by real-time RT-PCR. The grape *Actin1* and *EF1-α* genes were used as internal controls to normalize the data. *VvRD22*

served as a positive control for salt stress. The error bars were calculated based on three replicates.

Additional file 7: Expression patterns of grape AP genes under drought treatment. A. Expression patterns of 25 AP genes under drought treatment conditions were determined by semi-quantitative RT-PCR analyses. For each gene, the upper eight amplification bands represent amplified products from leaves of 'Kyoho' under drought stress for 24 h, 48 h, 72 h, 96 h, 120 h, 144 h, 168 h after 48 h of recovery (R48; rewatered); the bands under them represent amplified products from leaves of the control. B. Expression patterns of three randomly selected AP genes were detected by real-time PCR. *VvRD22* was used as a positive control.

Additional file 8: Expression patterns of grape AP genes under powdery mildew treatment. A. Expression patterns of 23 AP genes under PM treatment condition were determined by semi-quantitative RT-PCR analyses. For each gene, the upper seven amplification bands represent amplified products from leaves of 'Shang-24' after inoculation with powdery mildew; the bands under them represent amplified products from Mock-inoculated leaves. B. Expression patterns of three randomly selected AP genes were detected by real-time PCR. *VvPR1* was used as a positive control.

Additional file 9: Expression patterns of grape AP genes under SA treatment. A. Expression patterns of 25 AP genes under SA treatment conditions were determined by semi-quantitative RT-PCR analyses. For each gene, the upper seven amplification bands represent amplified products from leaves of 'Kyoho' after treatment with 100 μM SA; the bands under them represent amplified products from control leaves. B. Expression patterns of three randomly selected AP genes were analyzed by real-time PCR. *VvEDS1* was used as a positive control.

Additional file 10: Expression patterns of grape AP genes under ABA treatment. A. Expression patterns of 25 AP genes under ABA treatment conditions were determined by semi-quantitative RT-PCR analyses. For each gene, the upper seven amplification bands represent amplified products from leaves of 'Kyoho' after treatment with 100 μM ABA; the bands under them represent amplified products from control leaves. B. Expression patterns of three randomly selected AP genes were determined by real-time PCR. *VvCEF4* was used as a positive control.

Additional file 11: The cellular localization of grape APs.

Additional file 12: Comparison of expression pattern of orthologous AP pairs under various stresses and treatments.

Available expression patterns of *AtAP* genes based on microarray analysis and that of *VvAP* genes generated by semi-quantitative RT-PCR were compared.

Abbreviations

AP: Aspartic protease; CDR1: Constitutive disease resistance gene 1; PCS1: Promotion of cell survival gene 1; ASPG1: Aspartic protease in guard cell 1; WGD: Whole genome duplication; NJ: Neighbor-joining; SA: Salicylic acid; ABA: Abscissic acid; RT-PCR: Reverse transcription PCR; Hpt: Hours post-treatment; R48: 48-hour after rewatering; Hpi: Hours post-inoculation; PR: Pathogenesis-related; PCD: Programmed cell death.

Competing interests

The authors declare that they have no competing interests.

Authors' contributions

XW, RG designed the study. RG and YZ performed data analysis. XX, MG and XL contributed to abiotic and hormone treatments. RG and XL did the RT-PCR and qRT-PCR analysis. XW provided guidance on the whole study. RG and XW wrote and revised the manuscript. CLB assisted with the interpretation of the results and provided editorial support for the manuscript. All authors approved the final manuscript.

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